

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model.

Run on : August 19, 2003, 20:22:14 ; Search time 89 Seconds  
(without alignments) 167.360 Million cell updates/sec

Title: US-09-758-881-115

Perfect score: 20

Sequence: 1 gtcggacatctgtgtttc 20

Scoring table: IDNTRTY\_NUC

GapOp 10.0 , GapExt 1.0

Searched: 738101 seqs, 372376393 residues

Total number of hits satisfying chosen parameters: 567764

Minimum DB seq length: 9

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Pending\_Patents\_NA\_New:\*

1: /con2\_6/podata/2/pna/FCT\_NEW\_COMBO\_seq: \*  
2: /con2\_6/podata/2/pna/US06\_NEW\_COMBO\_seq: \*  
3: /con2\_6/podata/2/pna/US07\_NEW\_COMBO\_seq: \*  
4: /con2\_6/podata/2/pna/US08\_NEW\_COMBO\_seq: \*  
5: /con2\_6/podata/2/pna/US09\_NEW\_COMBO\_seq: \*  
6: /con2\_6/podata/2/pna/US10\_NEW\_COMBO\_seq: \*  
7: /con2\_6/podata/2/pna/US10\_NEW\_COMBO\_seq: \*

PRED. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	15.8	79.0	25	US-09-956-604D-50785
2	14.8	74.0	25	US-09-954-429-5485/C
3	14.4	72.0	25	US-09-956-604D-135640
4	14.2	71.0	25	US-09-956-604D-42506
5	14.2	71.0	25	US-10-318-855-17
6	13.8	69.0	25	US-09-956-604D-82056
7	13.8	69.0	25	US-09-956-604D-105387
8	13.8	69.0	25	US-10-367-832A-7968
9	13.6	68.0	23	US-10-367-832A-52667
10	13.6	68.0	25	US-09-954-429-10190
11	13.6	68.0	25	US-09-954-429-1884
12	13.4	67.0	16	US-10-367-832A-47439
13	13.4	67.0	22	US-10-367-832A-4424
14	13.4	67.0	23	US-10-367-832A-38748
15	13.4	67.0	24	US-10-367-832A-3541
16	13.4	67.0	25	US-09-956-604D-71887
17	13.4	67.0	25	US-09-954-429-843
18	13.4	67.0	25	US-09-956-604D-844
19	13.2	66.0	20	PCT-US03-16467-23
20	13.2	65.0	20	PCT-US03-16467-55
21	13.2	66.0	20	US-10-367-832A-37574
22	13.2	66.0	22	US-10-160-499-3369
23	13.2	66.0	24	PCT-US03-18714-31460
24	13.2	66.0	25	US-09-956-604D-73792
25	13.2	66.0	25	US-09-956-604D-73793

#### ALIGNMENTS

RESULT 1  
US-09-956-604D-50785  
; Sequence 50785, Application US/09956604D  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann, Michael  
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli  
; FILE REFERENCE: 3117.1  
; CURRENT APPLICATION NUMBER: US/09-956-604D  
; CURRENT FILING DATE: 2001-09-19  
; PRIOR APPLICATION NUMBER: 60/234,049  
; PRIOR FILING DATE: 2000-09-19  
; NUMBER OF SEQ ID NOS: 1,41629  
; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.2  
; SEQ ID NO 50785  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: E. coli

Query Match 79.0%; Score 15.8; DB 5; Length 25;  
Best Local Similarity 89.5%; Pred. No. 3.9e+02; Mismatches 2; Indels 0; Gaps 0;  
Matches 17; Conservative 0; Sequence 50785, A

Qy 1 GCTCCAGCATCTGCTGCTT 19  
Db 3 GCTCCAGCATCTGCTTCTT 21

RESULT 2  
US-09-954-429-5485/C  
; Sequence 5485, Application US/09954429  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann, Michael  
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat Neurobiology  
; FILE REFERENCE: 3114.1  
; CURRENT APPLICATION NUMBER: US/09-954-429  
; CURRENT FILING DATE: 2001-09-17  
; PRIOR APPLICATION NUMBER: 60/233,357  
; PRIOR FILING DATE: 2000-09-18  
; NUMBER OF SEQ ID NOS: 21305  
; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1  
; SEQ ID NO 5485  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus

Query Match 74.0%; Score 14.8; DB 5; Length 25;  
Best Local Similarity 88.9%; Pred. No. 1.1e+03;

RESULT 3  
; Sequence 135640, Application US/09956604D  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann, Michael  
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia Coli  
; FILE REFERENCE: 3117.1  
; CURRENT APPLICATION NUMBER: US/09/956, 604D  
; CURRENT FILING DATE: 2001-09-19  
; PRIOR APPLICATION NUMBER: 60/234, 049  
; PRIOR FILING DATE: 2000-09-19  
; NUMBER OF SEQ ID NOS: 141629  
; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.2  
; SEQ ID NO 135640  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: E. coli  
; US-09-956-604D-135640  
; Query Match 72.0%; Score 14.4; DB 5; Length 25;  
; Best Local Similarity 93.8%; Pred. No. 1.6e+03; Mismatches 0; Indels 0; Gaps 0;  
; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
; QY 1 GCTCAGGATCTGCTG 16  
; DB 9 GCTCCATATCTGCTG 24  
; RESULT 4  
; Sequence 42506, Application US/09956604D  
; GENERAL INFORMATION:  
; APPLICANT: Mittmann, Michael  
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia Coli  
; FILE REFERENCE: 3117.1  
; CURRENT APPLICATION NUMBER: US/09/956, 604D  
; CURRENT FILING DATE: 2001-09-19  
; PRIOR APPLICATION NUMBER: 60/234, 049  
; CURRENT FILING DATE: 2000-09-19  
; PRIOR APPLICATION NUMBER: US/09/956, 604D  
; NUMBER OF SEQ ID NOS: 141629  
; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.2  
; SEQ ID NO 42506  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: E. coli  
; US-09-956-604D-42506  
; Query Match 71.0%; Score 14.2; DB 5; Length 25;  
; Best Local Similarity 84.2%; Pred. No. 2e+03; Mismatches 0; Indels 0; Gaps 0;  
; Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
; QY 1 GTCAGGATCTGCTG 19  
; DB 3 GCTCCAGCTCTGGCT 21  
; RESULT 5  
; Sequence 10-318-825-17  
; Sequence 17, Application US/10318855  
; GENERAL INFORMATION:  
; APPLICANT: Vincent Ling  
; TITLE OF INVENTION: Novel GL50 MOLECULES AND USES THEREFOR  
; FILE REFERENCE: 3117.1  
; CURRENT APPLICATION NUMBER: US/10/318, 855  
; CURRENT FILING DATE: 2002-12-12  
; SEQ ID NO 105387  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: E. coli  
; US-09-956-604D-105387  
; Query Match 69.0%; Score 13.8; DB 5; Length 25;  
; Best Local Similarity 88.2%; Pred. No. 2.9e+03; Mismatches 2; Indels 0; Gaps 0;  
; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
; QY 1 GTCGCCACATCTGCTC 17

Db  
 RESULT 8  
 ; Sequence 7968, Application US/10367832A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
 ; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.  
 ; FILE REFERENCE: Jim Zeger Law Offices - 703-684-8333  
 ; CURRENT APPLICATION NUMBER: US/10/367,832A  
 ; CURRENT FILING DATE: 2002-08-26  
 ; NUMBER OF SEQ ID NOS: 64158  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 7968  
 ; LENGTH: 26  
 ; TYPE: DNA  
 ; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.  
 ; FEATURE:  
 ; LOCATION: (75258)..(75628)  
 ; OTHER INFORMATION: Chromosome - 1 Strand = negative ConnectronObjectNumber = 8554  
 ; US-10-367-832A-7968  
 Query Match 69.0%; Score 13.8; DB 6; Length 26;  
 Best Local Similarity 88.2%; Pred. No. 2.9e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 GCTCCAGCCTCTGTC 17  
 Db 25 GCTCCAGCCTCTGTC 9  
 ; LENGTH: 26  
 ; SEQ ID NO 7967  
 RESULT 9  
 ; Sequence 52967, Application US/10367832A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
 ; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.  
 ; FILE REFERENCE: Jim Zeger Law Offices - 703-684-8333  
 ; CURRENT APPLICATION NUMBER: US/10/367,832A  
 ; CURRENT FILING DATE: 2002-08-26  
 ; NUMBER OF SEQ ID NOS: 64158  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 52967  
 ; LENGTH: 23  
 ; TYPE: DNA  
 ; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.  
 ; FEATURE:  
 ; LOCATION: (515777)..(515779)  
 ; OTHER INFORMATION: Chromosome - 1 Strand = negative ConnectronObjectNumber = 56730  
 ; US-10-367-832A-52967  
 Query Match 68.0%; Score 13.6; DB 6; Length 23;  
 Best Local Similarity 80.0%; Pred. No. 3.e+03;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 GCTCCAGCCTCTGTC 20  
 Db 4 GCTCAAGCAGTGCCTTC 23  
 ; LENGTH: 23  
 ; SEQ ID NO 47439  
 RESULT 10  
 ; Sequence 10190, Application US/09954429  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mittmann, Michael  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Rat Neurobiology  
 ; FILE REFERENCE: 3114.1  
 ; CURRENT APPLICATION NUMBER: US/09/954,429  
 ; CURRENT FILING DATE: 2001-09-17  
 ; PRIOR APPLICATION NUMBER: 60/233,357  
 ; PRIOR FILING DATE: 2000-09-18  
 ; LENGTH: 23  
 ; SEQ ID NO 10190  
 ; NUMBER OF SEQ ID NOS: 21305  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 11884  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Rattus norvegicus  
 ; US-09-954-429-11884  
 Query Match 68.0%; Score 13.6; DB 5; Length 25;  
 Best Local Similarity 80.0%; Pred. No. 3.6e+03;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 GCTCCAGCCTCTGTC 25  
 Db 3 GCTCCAGCCTCTGCGGCTGC 22  
 ; LENGTH: 25  
 ; SEQ ID NO 11884  
 ; NUMBER OF SEQ ID NOS: 21305  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 11884  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Rattus norvegicus  
 ; US-09-954-429-11884  
 ; LENGTH: 25  
 ; SEQ ID NO 11884  
 ; NUMBER OF SEQ ID NOS: 21305  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 11884  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.  
 ; FEATURE:  
 ; LOCATION: (4596504)..(4596519)  
 ; OTHER INFORMATION: Chromosome - 1 Strand = positive ConnectronObjectNumber = 50  
 ; US-10-367-832A-47439  
 Query Match 67.0%; Score 13.4; DB 6; Length 16;  
 Best Local Similarity 93.3%; Pred. No. 4.3e+03;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 2 CTCCACATCTGCTG 16  
 Db 2 CTCACACCTTGCTG 16

